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Timestamp: [year=2010; month=5; day=13; hr=9; min=24; sec=47; ms=497;]

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Application No: 10594291 Version No: 2.0

Input Set:

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Started: 2010-05-07 10:39:51.149

Finished: 2010-05-07 10:39:52.191

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 42 ms

Total Warnings: 0

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No. of SeqIDs Defined: 18

Actual SeqID Count: 18

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Fraser, John David

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Lys Gln Glu Arg Val Gln His Leu His Asp Ile Arg Asp Leu His Arg
35 40 45

Tyr Tyr Ser Ser Glu Ser Phe Glu Tyr Ser Asn Val Ser Gly Lys Val
50 55 60

Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Pro Lys Asp Gln
65 70 75 80

Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Glu Gln Tyr Lys Glu
85 90 95

Gly Leu Gln Gly Gln Asn Val Phe Val Val Gln Glu Leu Ile Asp Pro
100 105 110

Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Lys
115 120 125

Thr Ser Glu Thr Asn Thr Pro Leu Phe Val Asn Lys Val Asn Gly Glu
130 135 140

Asp Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Gln Lys Glu Glu Ile
145 150 155 160

Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln Gln Leu Val Asn Asn
165 170 175

Tyr Gly Leu Tyr Lys Gly Thr Ser Lys Tyr Gly Lys Ile Ile Ile Asn
180 185 190

Leu Lys Asp Glu Asn Lys Val Glu Ile Asp Leu Gly Asp Lys Leu Gln
195 200 205

Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Arg Gly Ile
210 215 220

Ser Val Thr Ile Asn Gln Ile
225 230

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Lys Gln Glu Arg Val Gln His Leu His Asp Ile Arg Asp Leu His Arg
35 40 45

Tyr Tyr Ser Ser Glu Ser Phe Glu Tyr Ser Asn Val Ser Gly Lys Val
50 55 60

Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Pro Lys Asp Gln
65 70 75 80

Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Glu Gln Tyr Lys Glu
85 90 95

Gly Leu Gln Gly Gln Asn Val Phe Val Val Gln Glu Leu Ile Asp Pro
100 105 110

Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Lys
115 120 125

Thr Ser Glu Thr Asn Thr Pro Leu Phe Val Asn Lys Val Asn Gly Glu
130 135 140

Asp Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Gln Lys Glu Glu Ile
145 150 155 160

Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln Gln Leu Val Asn Asn
165 170 175

Tyr Gly Leu Tyr Lys Gly Thr Ser Lys Tyr Gly Lys Ile Ile Ile Asn
180 185 190

Leu Lys Asp Glu Asn Lys Val Glu Ile Asp Leu Gly Asp Lys Leu Gln
195 200 205

Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Arg Gly Ile
210 215 220

Ser Val Thr Ile Asn Gln Ile
225 230

<210> 3
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<212> PRT
<213> Staphylococcus aureus

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35 40 45

Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly Lys Val
50 55 60

Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu Lys Gln
65 70 75 80

Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Asp Lys Tyr Lys Lys
85 90 95

Gly Leu Glu Gly Gln Asn Val Phe Val Val Lys Glu Leu Ile Asp Pro
100 105 110

Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Lys
115 120 125

Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr Gly Gly
130 135 140

Asn Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Asn Lys Glu Glu Val
145 150 155 160

Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Gln Leu Val Glu Lys
165 170 175

Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr Ile Asn
180 185 190

Leu Lys Asp Glu Lys Lys Glu Val Ile Asp Leu Gly Asp Lys Leu Gln
195 200 205

Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Gln Asn Ile
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Ala Val Thr Ile Asn Gln Ile
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<213> Staphylococcus aureus

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Lys Gln Glu Arg Val Gln Glu Leu Tyr Asp Ile Lys Asp Leu Tyr Arg
35 40 45

Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly Lys Val
50 55 60

Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu Lys Gln
65 70 75 80

Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Asp Lys Tyr Lys Lys
85 90 95

Gly Leu Glu Gly Gln Asn Val Phe Val Val Lys Glu Leu Ile Asp Pro
100 105 110

Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Lys
115 120 125

Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr Gly Gly
130 135 140

Asn Leu Asp Ala Ser Ile Asp Ser Phe Leu Ile Asn Lys Glu Glu Val
145 150 155 160

Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Gln Leu Val Glu Lys
165 170 175

Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr Ile Asn
180 185 190

Leu Lys Asp Glu Lys Lys Glu Val Ile Asp Leu Gly Asp Lys Leu Gln
195 200 205

Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Gln Asn Ile
210 215 220

Ala Val Thr Ile Asn Gln Ile

225 230

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20 25 30

Lys Gln Glu Arg Val Gln His Leu Tyr Asp Ile Lys Asp Leu His Arg
35 40 45

Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly Lys Val
50 55 60

Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu Asn Gln
65 70 75 80

Asn His Gln Leu Phe Leu Ser Gly Lys Asp Lys Asp Lys Tyr Lys Glu
85 90 95

Gly Leu Glu Gly Gln Asn Val Phe Val Val Lys Glu Leu Ile Asp Pro
100 105 110

Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Gln
115 120 125

Ser Ser Glu Thr Asn Thr Pro Leu Phe Ile Lys Lys Val Tyr Gly Gly
130 135 140

Asn Leu Asp Ala Ser Ile Glu Ser Phe Leu Ile Asn Lys Glu Glu Val
145 150 155 160

Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln His Leu Val Lys Asn
165 170 175

Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr Phe Asn
180 185 190

Leu Lys Asp Gly Glu Lys Gln Glu Ile Asp Leu Gly Asp Lys Leu Gln
195 200 205

Phe Glu His Met Gly Asp Val Leu Asn Ser Lys Asp Ile Gln Asn Ile
210 215 220

Ala Val Thr Ile Asn Gln Ile
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<213> Staphylococcus aureus

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20 25 30

Lys Val Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Asp
35 40 45

Gly Gln Asn His Gln Leu Phe Leu Leu Gly Glu Asp Lys Ala Lys Tyr
50 55 60

Lys Gln Gly Leu Glu Gly Gln Asn Val Phe Val Val Lys Glu Leu Ile
65 70 75 80

Asp Pro Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn
85 90 95

Asn Gln Ser Ser Glu Thr Asn Thr Pro Leu Phe Val Lys Lys Val Tyr
100 105 110

Gly Gly Asn Leu Asp Ala Ser Ile Glu Ser Phe Ser Ile Asn Lys Glu
115 120 125

Glu Val Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln His Leu Val
130 135 140

Lys Asn Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr

145 150 155 160

Phe Asn Leu Lys Asp Gly Glu Lys Lys Glu Ile Asp Leu Gly Asp Lys
165 170 175

Leu Gln Phe Glu His Met Gly Asp Val Leu Asn Ser Lys Asp Ile Gln
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Asn Ile Ala Val Thr Leu Lys Gln Ile
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<210> 7
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His Arg Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly
20 25 30

Lys Val Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu
35 40 45

Lys Gln Asn His Gln Leu Phe Leu Leu Gly Glu Asp Lys Ala Lys Tyr
50 55 60

Lys Gln Gly Leu Gln Gly Gln Asp Val Phe Val Val Lys Glu Leu Ile
65 70 75 80

Asp Pro Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn
85 90 95

Asn Gln Ser Ser Glu Thr Asn Ile His Leu Leu Val Asn Lys Leu Asp
100 105 110

Gly Gly Asn Leu Asp Ala Thr Asn Asp Ser Phe Leu Ile Asn Lys Glu
115 120 125

Glu Val Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Gln Leu Val
130 135 140

Glu Lys Tyr Gly Leu Tyr Gln Gly Thr Ser Lys Tyr Gly Lys Ile Thr
 145 150 155 160

Ile Ile Leu Asn Gly Gly Lys Lys Gln Glu Ile Asp Leu Gly Asp Lys
 165 170 175

Leu Gln Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Asn
 180 185 190

Lys Ile Glu Val Thr Leu Lys Gln Ile
 195 200

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 catgatatta gagatttaca tcgatactac tcatcagaaa gtttcgaata tagtaatgtt 180
 agtggttaagg ttgaaaacta caatgggttct aacgttgttac gctttaaccc aaaagatcaa 240
 aatcaccaat tattcttatt aggaaaagat aaagaacaat ataaagaagg tctacaaggc 300
 caaaatgtct ttgtagtaca agaattaatt gatccaaaac gcagactatc tactgttggt 360
 ggtgtaacga agaaaaacaa caaaacttct gaaactaata cacctttatt tgttaataaa 420
 gttaatggtg aagattttaga tgcattcaatt gactcatttt taatccaaa agaagaaatc 480
 tcattaaaag agcttgattt caaaattaga caacaattag ttaataatta cggattatat 540
 aaaggtagat ctaaatacgg taaaatcatt atcaatttga aagacgaaaa taaagtagaa 600
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| tatgatatta aagacttata tcgatactac tcatcagaaa gttttgaatt cagtaatatt | 180 |
| agtggtaagg ttgaaaacta taacggttct aacgttgtac gctttaacca agaaaaacaa | 240 |
| aatcaccaat tattcttatt aggaaaagat aaagataaat ataaaaaagg ccttgaaggc | 300 |
| cagaatgtct ttgtggtaaa agaattaatt gatccaaacg gtagactatc tactgttggt | 360 |
| gggtgtgacta agaaaaataa caaatcttct gaaactaata cacatttatt tgttaataaa | 420 |
| gtgtatggcg gaaatttaga tgcatacaatt gactcatttt taattaataa agaagaagtt | 480 |
| tcactgaaag aacttgattt caaaattaga aagcaattag ttgaaaaata tggtttatat | 540 |
| aaagggtacga ctaaatacgg taagatcact atcaatttga aagacgagaa aaaggaagta | 600 |
| attgatttag gtgataaact gcaattcgag cgcattgggtg atgtgttgaa tagtaaggat | 660 |
| attcaaaata tagcagtgac tattaatcaa atttaa | 696 |

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 <212> DNA
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| attacatcag aaggccaagc agtccacgca aaagaaaagc aagagagagt acaacattta | 120 |
| tatgatatta aagacttata tcgatactac tcatcagaaa gttttgaatt cagtaatatt | 180 |
| agtggtaagg ttgaaaacta taacggttct aacgttgtac gctttaacca agaaaaacaa | 240 |
| aatcaccaat tattcttatt aggaaaagat aaagataaat ataaaaaagg ccttgaaggc | 300 |
| cagaatgtct ttgtggtaaa agaattaatt gatccaaacg gtagactatc tactgttggt | 360 |
| gggtgtgacta agaaaaataa caaatcttct gaaactaata cacatttatt tgttaataaa | 420 |
| gtgtatggcg gaaatttaga tgcatacaatt gactcatttt taattaataa agaagaagtt | 480 |
| tcactgaaag aacttgattt caaaattaga aagcaattag ttgaaaaata tggtttatat | 540 |
| aaagggtacga ctaaatacgg taagatcact atcaatttga aagacgagaa aaaggaagta | 600 |
| attgatttag gtgataaact gcaattcgag cgcattgggtg atgtgttgaa tagtaaggat | 660 |
| attcaaaata tagcagtgac tattaatcaa atttaa | 696 |

<210> 11
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<400> 11

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| attacatcag aaggccaagc agtgcaagca aaagaaaagc aagagagagt acaacattta | 120 |
| tatgatatta aagacttaca tcgatactac tcatcagaaa gttttgaatt cagtaatatt | 180 |
| agtggttaagg ttgaaaatta taacggttct aacgttgtag gctttaacca agaaaatcaa | 240 |
| aatcaccaat tattcttattc aggaaaagat aaagataaat ataaagaagg ccttgaaggc | 300 |
| cagaatgtct ttgtggtaaa agaattaatt gatccaaacg gtagactatc tactgttggg | 360 |
| ggtgtaac | |